SEQUENCE LISTING

<110> Human Genome Sciences, Inc.

<120> Albumin Fusion Proteins

<130> PF544PCT

<140> Unassigned
<141> 2001-04-12

<150> 60/229,358
<151> 2000-04-12

<150> 60/256,931
<151> 2000-12-21

<150> 60/199,384
<151> 2000-04-25

<160> 45

<170> PatentIn Ver. 2.1

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gataaagatt cccaac                                              16


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with non-cohesive ends.

<400> 5
ttaggcttat tcccaac                                            17


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with non-cohesive ends.
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<400> 7
Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
  1   5   10   15

Ile Ser Ala Asp Ala His Lys Ser
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<213> Artificial Sequence

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fragments with non-cohesive ends.

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fragments with non-cohesive ends.

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<210> 14
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<400> 14
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fragments with non-cohesive ends.

<400> 15
ttaggcttag gcggtggtgg atctggtggc ggcggatctg gtggcggtgg atccttccca 60
ac   62

<210> 16
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Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1               5                   10                  15

gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag     96
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa    144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa    192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt    240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct    288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc    336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat    384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga    432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg    480
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Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145             150             155                 160

tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc   528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165             170             175

tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg   576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
                180             185             190

tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa   624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
            195             200             205

aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc   672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
        210             215             220

aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa   720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225             230             235             240

gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac   768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245             250             255

agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc   816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260             265             270

agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac   864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
            275             280             285

tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca   912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290             295             300

tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct   960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305             310             315             320

gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga  1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325             330             335

agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca  1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340             345             350
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7

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tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa   1104
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct   1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
        370                 375                 380

cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag   1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc   1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa   1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
                420                 425                 430

gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt   1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
                435                 440                 445

gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat   1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
        450                 455                 460

gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc   1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca   1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat   1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
                500                 505                 510

ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca   1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg   1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
        530                 535                 540

aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag   1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560
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8

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gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt   1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565             570             575


gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag  1782
Ala Ala Ser Gln Ala Ala Leu Gly Leu
                580             585



<210> 18
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<213> Homo Sapiens


<400> 18
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
  1               5               10              15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20              25              30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35              40              45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50              55              60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65              70              75              80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85              90              95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100             105             110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115             120             125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
        130             135             140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145             150             155             160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165             170             175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
                180             185             190
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9

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195   200   205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210   215   220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225   230   235   240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245   250   255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
        260   265   270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275   280   285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290   295   300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305   310   315   320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325   330   335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340   345   350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355   360   365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370   375   380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385   390   395   400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
            405   410   415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420   425   430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435   440   445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450   455   460

10

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465   470   475   480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485   490   495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500   505   510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515   520   525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530   535   540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545   550   555   560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
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Ala Ala Ser Gln Ala Ala Leu Gly Leu
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site in pPPC0006

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site in pPPC0006

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sites in pPPC0007

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sites in pPPC0007

<400> 24
agaattaagc ttagtttaaa cggccggccg gcgcgcctta ttataagcct aaggcagctt 60

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<223> forward primer useful for generation of albumin
fusion protein in which the albumin moiety is N-terminal
of the Therapeutic Protein

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protein in which the albumin  moiety is c-terminal of the
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<222> (49)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (50)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (51)
<223> n equals a,t,g, or c
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<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c

<400> 28
ctttaaatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnnn nn   52

<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> signal peptide of natural human serum albumin protein

<400> 29
Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
  1   5   10   15

Tyr Ser Arg Ser Leu Asp Lys Arg
            20

<210> 30
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of PC4:HSA
albumin fusion VECTOR

<220>
<221> misc_feature
<222> (5)..(10)
<223> BamHI retsriction site

<220>
<221> misc_feature
<222> (11)..(16)
<223> Hind III retsriction site

<220>
<221> misc_feature
<222> (17)..(27)
<223> Kozak sequence

<220>
<221> misc_feature
<222> (25)..(97)
<223> cds natural signal sequence of human serum albumin

<220>
<221> misc_feature
<222> (75)..(81)
<223> XhoI restriction site

<220>
<221> misc_feature
<222> (98)..(114)
<223> cds first six amino acids of human serum albumin

<400> 30
tcagggatcc aagcttccgc caccatgaag tgggtaacct ttatttccct tctttttctc 60

tttagctcgg cttactcgag gggtgtgttt cgtcgagatg cacacaagag tgag   114

<210> 31
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of
PC4:HSA albumin fusion VECTOR

<220>
<221> misc_feature
<222> (6)..(11)
<223> Asp718 restriction site

<220>
<221> misc_feature
<222> (12)..(17)
<223> EcoRI restriction site

<220>
<221> misc_feature
<222> (15)..(17)
<223> reverse complement of stop codon

<220>
<221> misc_feature
<222> (18)..(25)
<223> AscI restriction site

```
<220>
<221> misc_feature
<222> (18)..(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

<400> 31
gcagcggtac cgaattcggc gcgccttata agcctaaggc agc                          43

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for inserting Therapeutic
protein into pC4:HSA vector

<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (31)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (33)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (34)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (35)
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<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (37)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (39)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c
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<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<400> 32
ccgccgctcg aggggtgtgt ttcgtcgann nnnnnnnnnn nnnnnn                    46

<210> 33
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for inserting Therapeutic
protein into pC4:HSA vector

<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (39)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
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<222> (44)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (47)
<223> n.equals a,t,g, or c


<220>
<221> misc feature
<222> (48)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (49)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (50)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (51)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (53)
<223> n equals a,t,g, or c


<220>
<221> misc feature
<222> (54)
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<400> 33
agtcccatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnn nnnnn   55

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Stanniocalcin signal peptide

<400> 34
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Leu Val Ile Ser Ala Ser
 1   5   10   15

Ala

<210> 35
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Synthetic signal peptide

<400> 35
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
 1   5   10   15

Trp Ala Pro Ala Arg Gly
            20

<210> 36
<211> 733
<212> DNA
<213> Homo sapiens

<400> 36
gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg   60

aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaggac accctcatga   120

```
tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg      180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg      240

aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact      300

ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg      360

agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc      420

catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct      480

atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga      540

ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg      600

acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc      660

acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc      720

gactctagag gat                                                        733


<210> 37
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<221> misc_structure
<223> membrane proximal motif of class 1 cytokine receptors

<220>
<221> misc_feature
<222> (3)
<223> Xaa equals any


<400> 37
Trp Ser Xaa Trp Ser
  1               5

<210> 38
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element
```

```
<400> 38
gcgcctcgag atttccccga atctagatt tccccgaaat gatttccccg aaatgatttc        60

cccgaaatat ctgccatctc aattag                                            86

<210> 39
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element

<400> 39
gcggcaagct ttttgcaaag cctaggc                                           27

<210> 40
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Synthetic GAS-SV40 promoter sequence

<400> 40
ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg        60

aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc       120

gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat        180

ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt        240

ttttggaggc ctaggctttt gcaaaaagct t                                      271

<210> 41
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 41
gcgctcgagg gatgacagcg atagaacccc gg                                     32
```

```
<210> 42
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 42
gcgaagcttc gcgactcccc ggatccgcct c                                31


<210> 43
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_binding
<223> NF-KB binding site

<400> 43
ggggactttc cc                                                     12


<210> 44
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of a vector containing the
NF-KB promoter element

<400> 44
gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg   60

ccatctcaat tag                                                    73



<210> 45
<211> 256
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Synthetic NF-KB/SV40 promoter

<400> 45
ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct   60
```

```
caattagtca gcaaccatag tcccgcccct aactccgccc atcccgcccc taactccgcc      120

cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga      180

ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg      240

cttttgcaaa aagctt                                                      256
```